RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/591,432_
Source: _1 FWP_
Date Processed by STIC: _9/13/06_

ENTERED

IFWP

RAW SEQUENCE LISTING   DATE: 09/13/2006
PATENT APPLICATION: US/10/591,432   TIME: 13:16:43

Input Set : **N:\RJAVED\10591432.txt**
Output Set: **N:\CRF4\09132006\J591432.raw**

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     3 <110> APPLICANT: Frohberg, Claus
     4         Koetting, Oliver
     5         Ritte, Gerhard
     6         Steup, Martin
     8 <120> TITLE OF INVENTION: Plants with increased activity of multiple starch
phosphorylating enzymes
    10 <130> FILE REFERENCE: 65084.000022
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/591,432
    13 <141> CURRENT FILING DATE: 2006-09-01
    15 <150> PRIOR APPLICATION NUMBER: EP 04090089.6
    16 <151> PRIOR FILING DATE: 2004-03-05
    18 <150> PRIOR APPLICATION NUMBER: US 60/550,021
    19 <151> PRIOR FILING DATE: 2004-03-05
    21 <150> PRIOR APPLICATION NUMBER: EP 04090284.3
    22 <151> PRIOR FILING DATE: 2004-07-21
    24 <150> PRIOR APPLICATION NUMBER: EP 04090121.7
    25 <151> PRIOR FILING DATE: 2004-03-29
    27 <160> NUMBER OF SEQ ID NOS: 39
    29 <170> SOFTWARE: PatentIn version 3.1
    31 <210> SEQ ID NO: 1
    32 <211> LENGTH: 3591
    33 <212> TYPE: DNA
    34 <213> ORGANISM: Arabidopsis thaliana
    36 <220> FEATURE:
    37 <221> NAME/KEY: CDS
    38 <222> LOCATION: (1)..(3591)
    39 <223> OTHER INFORMATION:
W--> 42 <400> 1
    43 atg gag agc att ggc agc cat tgt tgc agc tct cct ttc acc ttc atc       48
    44 Met Glu Ser Ile Gly Ser His Cys Cys Ser Ser Pro Phe Thr Phe Ile
    45 1               5                   10                  15
    47 act aga aac tca tca tca tca ctt cct aga ctc gtt aac atc act cac       96
    48 Thr Arg Asn Ser Ser Ser Ser Leu Pro Arg Leu Val Asn Ile Thr His
    49             20                  25                  30
    51 aga gtt aat ctc agc cac caa tct cac cga ctc aga aac tcc aat tct      144
    52 Arg Val Asn Leu Ser His Gln Ser His Arg Leu Arg Asn Ser Asn Ser
    53             35                  40                  45
    55 cgt ctc act tgc act gct act tct tct tcc acc att gag gaa caa cgg      192
    56 Arg Leu Thr Cys Thr Ala Thr Ser Ser Ser Thr Ile Glu Glu Gln Arg
    57         50                  55                  60
    59 aag aag aaa gat gga tca gga acg aaa gtg agg ttg aat gtg agg tta      240
    60 Lys Lys Lys Asp Gly Ser Gly Thr Lys Val Arg Leu Asn Val Arg Leu
    61 65                  70                  75                  80
    63 gat cat caa gtt aat ttt ggt gac cat gtg gct atg ttt gga tca gct      288
```

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64 Asp His Gln Val Asn Phe Gly Asp His Val Ala Met Phe Gly Ser Ala
65               85                90                95
67 aaa gag att ggt tca tgg aaa aag aaa tcg cct ttg aat tgg agt gag      336
68 Lys Glu Ile Gly Ser Trp Lys Lys Lys Ser Pro Leu Asn Trp Ser Glu
69               100               105               110
71 aat gga tgg gtt tgt gag ttg gaa ctt gac ggt ggt cag gtt ttg gag      384
72 Asn Gly Trp Val Cys Glu Leu Glu Leu Asp Gly Gly Gln Val Leu Glu
73               115               120               125
75 tat aag ttt gtc att gtt aag aat gat ggt tca ctt tca tgg gaa tct      432
76 Tyr Lys Phe Val Ile Val Lys Asn Asp Gly Ser Leu Ser Trp Glu Ser
77     130               135               140
79 ggt gat aat cgt gtc ctt aag gtt cca aat tct ggg aat ttt tct gtt      480
80 Gly Asp Asn Arg Val Leu Lys Val Pro Asn Ser Gly Asn Phe Ser Val
81 145               150               155               160
83 gtt tgt cat tgg gat gct act aga gaa acc ctt gat ttg cct cag gag      528
84 Val Cys His Trp Asp Ala Thr Arg Glu Thr Leu Asp Leu Pro Gln Glu
85               165               170               175
87 gtt ggt aat gat gat gat gtt ggt gat ggt ggg cat gag agg gat aat      576
88 Val Gly Asn Asp Asp Asp Val Gly Asp Gly Gly His Glu Arg Asp Asn
89               180               185               190
91 cat gat gtt ggt gat gat aga gta gtg gga agt gaa aat ggt gcg cag      624
92 His Asp Val Gly Asp Asp Arg Val Val Gly Ser Glu Asn Gly Ala Gln
93               195               200               205
95 ctt cag aag agt aca ttg ggt ggg caa tgg caa ggt aaa gat gcg tcc      672
96 Leu Gln Lys Ser Thr Leu Gly Gly Gln Trp Gln Gly Lys Asp Ala Ser
97     210               215               220
99 ttt atg cgt tct aat gat cat ggt aac aga gaa gtt ggt aga aat tgg      720
100 Phe Met Arg Ser Asn Asp His Gly Asn Arg Glu Val Gly Arg Asn Trp
101 225               230               235               240
103 gat act agt ggt ctt gaa ggc aca gct ctt aag atg gtt gag ggt gat     768
104 Asp Thr Ser Gly Leu Glu Gly Thr Ala Leu Lys Met Val Glu Gly Asp
105               245               250               255
107 cgc aac tct aag aac tgg tgg aga aag ctt gaa atg gta cgc gag gtt     816
108 Arg Asn Ser Lys Asn Trp Trp Arg Lys Leu Glu Met Val Arg Glu Val
109               260               265               270
111 ata gtt ggg agt gtt gag agg gag gaa cga ttg aag gcg ctc ata tac     864
112 Ile Val Gly Ser Val Glu Arg Glu Glu Arg Leu Lys Ala Leu Ile Tyr
113               275               280               285
115 tct gca att tat ttg aag tgg ata aac aca ggt cag att cct tgt ttt     912
116 Ser Ala Ile Tyr Leu Lys Trp Ile Asn Thr Gly Gln Ile Pro Cys Phe
117     290               295               300
119 gaa gat gga ggg cat cac cgt cca aac agg cat gcc gag att tcc aga     960
120 Glu Asp Gly Gly His His Arg Pro Asn Arg His Ala Glu Ile Ser Arg
121 305               310               315               320
123 ctt ata ttc cgt gag ttg gag cac att tgc agt aag aaa gat gct act    1008
124 Leu Ile Phe Arg Glu Leu Glu His Ile Cys Ser Lys Lys Asp Ala Thr
125               325               330               335
127 cca gag gaa gtg ctt gtt gct cgg aaa atc cat ccg tgt tta cct tct    1056
128 Pro Glu Glu Val Leu Val Ala Arg Lys Ile His Pro Cys Leu Pro Ser
```

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Input Set : **N:\RJAVED\10591432.txt**
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129               340               345               350
131 ttc aaa gca gag ttt act gca gct gtc cct cta act cgg att agg gac     1104
132 Phe Lys Ala Glu Phe Thr Ala Ala Val Pro Leu Thr Arg Ile Arg Asp
133         355               360               365
135 ata gcc cat cgg aat gat att cct cat gat ctc aag caa gaa atc aag     1152
136 Ile Ala His Arg Asn Asp Ile Pro His Asp Leu Lys Gln Glu Ile Lys
137     370               375               380
139 cat acg ata caa aat aag ctt cac cgg aat gct ggt cca gaa gat cta     1200
140 His Thr Ile Gln Asn Lys Leu His Arg Asn Ala Gly Pro Glu Asp Leu
141 385               390               395               400
143 att gca aca gaa gca atg ctt caa cga att acc gag acc cca gga aaa     1248
144 Ile Ala Thr Glu Ala Met Leu Gln Arg Ile Thr Glu Thr Pro Gly Lys
145               405               410               415
147 tat agt gga gac ttt gtg gag cag ttt aaa ata ttc cat aat gag ctt     1296
148 Tyr Ser Gly Asp Phe Val Glu Gln Phe Lys Ile Phe His Asn Glu Leu
149           420               425               430
151 aaa gat ttc ttt aat gct gga agt ctc act gaa cag ctt gat tct atg     1344
152 Lys Asp Phe Phe Asn Ala Gly Ser Leu Thr Glu Gln Leu Asp Ser Met
153         435               440               445
155 aaa att tct atg gat gat aga ggt ctt tct gcg ctc aat ttg ttt ttt     1392
156 Lys Ile Ser Met Asp Asp Arg Gly Leu Ser Ala Leu Asn Leu Phe Phe
157     450               455               460
159 gaa tgt aaa aag cgc ctt gac aca tca gga gaa tca agc aat gtt ttg     1440
160 Glu Cys Lys Lys Arg Leu Asp Thr Ser Gly Glu Ser Ser Asn Val Leu
161 465               470               475               480
163 gag ttg att aaa acc atg cat tct cta gct tct tta aga gaa aca att     1488
164 Glu Leu Ile Lys Thr Met His Ser Leu Ala Ser Leu Arg Glu Thr Ile
165               485               490               495
167 ata aag gaa ctt aat agc ggc ttg cga aat gat gct cct gat act gcc     1536
168 Ile Lys Glu Leu Asn Ser Gly Leu Arg Asn Asp Ala Pro Asp Thr Ala
169         500               505               510
171 att gca atg cgc cag aag tgg cgc ctt tgt gag atc ggc ctc gag gac     1584
172 Ile Ala Met Arg Gln Lys Trp Arg Leu Cys Glu Ile Gly Leu Glu Asp
173         515               520               525
175 tac ttt ttt gtt cta cta agc aga ttc ctc aat gct ctt gaa act atg     1632
176 Tyr Phe Phe Val Leu Leu Ser Arg Phe Leu Asn Ala Leu Glu Thr Met
177     530               535               540
179 gga gga gct gat caa ctg gca aaa gat gtg gga tca aga aac gtt gcc     1680
180 Gly Gly Ala Asp Gln Leu Ala Lys Asp Val Gly Ser Arg Asn Val Ala
181 545               550               555               560
183 tca tgg aat gat cca cta gat gct ttg gtg ttg ggt gtt cac caa gta     1728
184 Ser Trp Asn Asp Pro Leu Asp Ala Leu Val Leu Gly Val His Gln Val
185               565               570               575
187 ggt cta tct ggt tgg aag caa gaa gaa tgt tta gcc att gga aat gaa     1776
188 Gly Leu Ser Gly Trp Lys Gln Glu Glu Cys Leu Ala Ile Gly Asn Glu
189         580               585               590
191 ctc ctt gct tgg cga gaa agg gac cta ctt gaa aaa gaa ggg gaa gag     1824
192 Leu Leu Ala Trp Arg Glu Arg Asp Leu Leu Glu Lys Glu Gly Glu Glu
193         595               600               605
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195 gat gga aaa aca att tgg gcc atg agg ctg aaa gca act ctt gat cga    1872
196 Asp Gly Lys Thr Ile Trp Ala Met Arg Leu Lys Ala Thr Leu Asp Arg
197     610             615             620
199 gca cgc aga tta aca gca gaa tat tct gat ttg ctt ctt caa ata ttt    1920
200 Ala Arg Arg Leu Thr Ala Glu Tyr Ser Asp Leu Leu Leu Gln Ile Phe
201 625             630             635             640
203 cct cct aat gtg gag att tta gga aaa gct cta gga att cca gag aat    1968
204 Pro Pro Asn Val Glu Ile Leu Gly Lys Ala Leu Gly Ile Pro Glu Asn
205             645             650             655
207 agt gtc aag acc tat aca gaa gca gag att cgt gct gga att att ttc    2016
208 Ser Val Lys Thr Tyr Thr Glu Ala Glu Ile Arg Ala Gly Ile Ile Phe
209             660             665             670
211 cag atc tca aag ctc tgc act gtt ctt cta aaa gct gta aga aat tca    2064
212 Gln Ile Ser Lys Leu Cys Thr Val Leu Leu Lys Ala Val Arg Asn Ser
213             675             680             685
215 ctt ggt tct gag ggc tgg gat gtc gtt gta cct gga tcg acg tct ggg    2112
216 Leu Gly Ser Glu Gly Trp Asp Val Val Val Pro Gly Ser Thr Ser Gly
217     690             695             700
219 aca tta gtt cag gtt gag agc att gtt ccg gga tca ttg cca gca act    2160
220 Thr Leu Val Gln Val Glu Ser Ile Val Pro Gly Ser Leu Pro Ala Thr
221 705             710             715             720
223 tct ggt ggt cct att att ctc ttg gtc aat aaa gct gat ggc gat gaa    2208
224 Ser Gly Gly Pro Ile Ile Leu Leu Val Asn Lys Ala Asp Gly Asp Glu
225             725             730             735
227 gag gta agt gct gct aat ggg aac ata gct gga gtc atg ctt ctg cag    2256
228 Glu Val Ser Ala Ala Asn Gly Asn Ile Ala Gly Val Met Leu Leu Gln
229             740             745             750
231 gag ctg cct cac ttg tct cac ctt ggc gtt aga gcg cgg cag gag aaa    2304
232 Glu Leu Pro His Leu Ser His Leu Gly Val Arg Ala Arg Gln Glu Lys
233     755             760             765
235 att gtc ttt gtg aca tgt gat gat gat gac aag gtt gct gat ata cga    2352
236 Ile Val Phe Val Thr Cys Asp Asp Asp Asp Lys Val Ala Asp Ile Arg
237     770             775             780
239 cga ctt gtg gga aaa ttt gtg agg ttg gaa gca tct cca agt cat gtg    2400
240 Arg Leu Val Gly Lys Phe Val Arg Leu Glu Ala Ser Pro Ser His Val
241 785             790             795             800
243 aat ctg ata ctt tca act gag ggt agg agt cgc act tcc aaa tcc agt    2448
244 Asn Leu Ile Leu Ser Thr Glu Gly Arg Ser Arg Thr Ser Lys Ser Ser
245             805             810             815
247 gcg acc aaa aaa acg gat aag aac agc tta tct aag aaa aaa aca gat    2496
248 Ala Thr Lys Lys Thr Asp Lys Asn Ser Leu Ser Lys Lys Lys Thr Asp
249             820             825             830
251 aag aag agc tta tct atc gat gat gaa gaa tca aag cct ggt tcc tca    2544
252 Lys Lys Ser Leu Ser Ile Asp Asp Glu Glu Ser Lys Pro Gly Ser Ser
253             835             840             845
255 tct tcc aat agc ctc ctt tac tct tcc aag gat atc cct agt gga gga    2592
256 Ser Ser Asn Ser Leu Leu Tyr Ser Ser Lys Asp Ile Pro Ser Gly Gly
257     850             855             860
259 atc ata gca ctt gct gat gca gat gta cca act tct ggt tca aaa tct    2640
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Input Set : **N:\RJAVED\10591432.txt**
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260 Ile Ile Ala Leu Ala Asp Ala Asp Val Pro Thr Ser Gly Ser Lys Ser
261 865                 870                 875                 880
263 gct gca tgt ggt ctt ctt gca tct tta gca gaa gcc tct agt aaa gtg    2688
264 Ala Ala Cys Gly Leu Leu Ala Ser Leu Ala Glu Ala Ser Ser Lys Val
265                 885                 890                 895
267 cac agc gaa cac gga gtt ccg gca tca ttt aag gtt cca act gga gtt    2736
268 His Ser Glu His Gly Val Pro Ala Ser Phe Lys Val Pro Thr Gly Val
269             900                 905                 910
271 gtc ata cct ttt gga tcg atg gaa tta gct tta aag caa aat aat tcg    2784
272 Val Ile Pro Phe Gly Ser Met Glu Leu Ala Leu Lys Gln Asn Asn Ser
273         915                 920                 925
275 gaa gaa aag ttt gcg tct ttg cta gaa aaa cta gaa acc gcc aga cct    2832
276 Glu Glu Lys Phe Ala Ser Leu Leu Glu Lys Leu Glu Thr Ala Arg Pro
277     930                 935                 940
279 gag ggt ggt gag cta gac gac ata tgt gac cag atc cat gaa gtg atg    2880
280 Glu Gly Gly Glu Leu Asp Asp Ile Cys Asp Gln Ile His Glu Val Met
281 945                 950                 955                 960
283 aaa acg ttg caa gtg cct aaa gaa aca atc aac agc ata agc aaa gcg    2928
284 Lys Thr Leu Gln Val Pro Lys Glu Thr Ile Asn Ser Ile Ser Lys Ala
285                 965                 970                 975
287 ttt ctc aaa gat gct cgt ctc att gtt cgt tca agt gct aac gtc gag    2976
288 Phe Leu Lys Asp Ala Arg Leu Ile Val Arg Ser Ser Ala Asn Val Glu
289         980                 985                 990
291 gac tta gcc gga atg tca gct gca  gga ctc tat gaa tca  atc cct aac    3024
292 Asp Leu Ala Gly Met Ser Ala Ala  Gly Leu Tyr Glu Ser  Ile Pro Asn
293         995                 1000                1005
295 gtg agt  ccc tcg gat cct ttg  gtg ttt tca gat tcg  gtt tgc caa    3069
296 Val Ser  Pro Ser Asp Pro Leu  Val Phe Ser Asp Ser  Val Cys Gln
297     1010                1015                1020
299 gtt tgg  gct tct ctc tac aca  aga aga gct gtt cta  agc cgt aga    3114
300 Val Trp  Ala Ser Leu Tyr Thr  Arg Arg Ala Val Leu  Ser Arg Arg
301     1025                1030                1035
303 gct gct  ggt gtc tct caa aga  gaa gct tca atg gct  gtt ctc gtt    3159
304 Ala Ala  Gly Val Ser Gln Arg  Glu Ala Ser Met Ala  Val Leu Val
305     1040                1045                1050
307 caa gaa  atg ctt tcg ccg gac  tta tca ttc gtt ctg  cac aca gtg    3204
308 Gln Glu  Met Leu Ser Pro Asp  Leu Ser Phe Val Leu  His Thr Val
309     1055                1060                1065
311 agt cca  gct gat ccg gac agt  aac ctt gtg gaa gcc  gag atc gct    3249
312 Ser Pro  Ala Asp Pro Asp Ser  Asn Leu Val Glu Ala  Glu Ile Ala
313     1070                1075                1080
315 cct ggt  tta ggt gag act tta  gct tca gga aca aga  gga aca cca    3294
316 Pro Gly  Leu Gly Glu Thr Leu  Ala Ser Gly Thr Arg  Gly Thr Pro
317     1085                1090                1095
319 tgg aga  ctc gct tcg ggt aag  ctc gac ggg att gta  caa acc tta    3339
320 Trp Arg  Leu Ala Ser Gly Lys  Leu Asp Gly Ile Val  Gln Thr Leu
321     1100                1105                1110
323 gct ttc  gca aac ttc agc gaa  gag ctt ctt gtg tca  gga aca ggt    3384
324 Ala Phe  Ala Asn Phe Ser Glu  Glu Leu Leu Val Ser  Gly Thr Gly
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 09/13/2006
PATENT APPLICATION: **US/10/591,432**   TIME: 13:16:44

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<u>**Invalid Line Length:**</u>
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 8

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:42 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:39
L:670 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:667
L:1321 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:1314
L:2127 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:2120
L:2871 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:2864
L:3665 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:3658
L:4443 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:4436
L:5231 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:5224
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